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Human-Murine Chimeric Antibodies Against Respiratory Syncytial Virus

Ins A1

BACKGROUND

This application is a continuation-in-part of U.S. Application Serial No. 07/813,372, filed on December 23, 1991.

Respiratory syncytial virus (RSV) is the major cause of acute respiratory illness in young children admitted to hospitals, and the community practice will treat perhaps five times the number of hospitalized children. It is therefore, the most common cause of lower respiratory tract infection in young children. While the majority of community-acquired RSV infections resolve themselves in a week to ten days, many hospitalized children, especially under six months of age require assisted ventilation.

Efforts to produce an effective vaccine have been unsuccessful (8). A major obstacle to vaccine development is safety; the initial formalin inactivated RSV vaccine caused an increased incidence of RSV lower respiratory tract disease and death in immunized children upon exposure to virus (5).

Recently, the drug ribavirin has been licensed for therapy of RSV pneumonia and bronchiolitis (2,3); its value is contraversial (4). Although ribavirin has shown efficacy (9), the drug has to be

administer d over an 18 hour period by aerosol inhalation. In addition, the level of secondary infections following c ssation of treatment is significantly higher than in untreated patients.

Studies have shown that high-titered RSV immunoglobulin was effective both in prophylaxis and therapy for RSV infections in animal models (6, 7). Infected animals treated with RSV immune globulin, showed no evidence of pulmonary immune-complex disease (6, 7).

Even if RSV hyperimmune globulin is shown to reduce the incidence and severity of RSV lower respiratory tract infection in high risk children, several disadvantages may limit its use. One drawback is the necessity for intravenous infusion in these children who have limited venous access because of prior intensiv therapy. A second disadvantage is the large volume of RSVIG required for protection, particularly since most these children have compromised cardiopulmonary function. A third disadvantage is that intravenous infusion necessitates monthly hospital visits during the RSV season which places these children at risk of nosocomial RSV infection (1). A final problem is that it may prove to be very difficult to select sufficient donors to produce a hyperimmune globulin for RSV to meet the demand for this product. Currently only about 8% of normal donors have RSV neutralizing antibody titers high enough to qualify for the production of hyperimmune globulin.

Another approach may be the development of monoclonal antibodies with high specific neutralizing activity as an alternative to hyperimmune globulin. It is preferable, if not necessary, to use human monoclonal antibodies rather than murine or rat antibodies to minimize the development of human anti-rodent antibody responses which may compromise the therapeutic efficacy of the antibody or induce immune-complex pathology. However, the generation of human monoclonal antibodies with the desired specificity may be difficult and the level of production from human cell lines is often low, precluding th ir dev lopment.

An alternativ approach involves the production of human-mouse chimeric antibodies in which the genetic information encoding the murine heavy and light chain variable regions are fixed to genes encoding the human heavy and light constant regions. The resulting mouse-human hybrid has about 30% of the intact immunoglobulin derived from murine sequences. Therefore, although a number of laboratories have constructed chimeric antibodies with mouse variable and human constant domains (10-18), the mouse variable region may still be seen as foreign (19).

SUMMARY OF THE INVENTION

It is therefore an object of the present invention to provide a complementarity determining region (CDR)-grafted human antibody which contains at least one CDR from each variable heavy chain and variable light chain of at least one monoclonal antibody, against the RSV antigen. The monoclonal antibody may be derived from any non-human animal, preferably howver, it is derived from a rodent and most preferably it is a murine monoclonal antibody. Preferably, the murine monoclonal antibody is a neutralizing antibody. It is also preferable that said murine antibody is an antibody against RSV F antigen.

The term "animal" as used herein is used in its broadest sense includes mammals including humans.

DETAILED DESCRIPTION OF THE DRAWINGS

The drawings depicted and described herein are intended to further illustrate the present invention and are not intended to limit the invention in any manner whatsoever.

Figure 1 shows the amino acid (AA) sequence design of CDR-Grafted anti-RSV F glycoprotein V_H. The figure depicts the AA sequence for the human HV3 V_H before grafting (SEQ ID NO:16), CDR grafted V_H (SEQ ID NO:17), and murine MAb1308F V_H (SEQ ID NO:18) from which the CDR sequence was grafted. The heavily underlined regions identify the CDR sequence which was

grafted into the human HV3 V_H and each of the thre regions is identified as CDR1, CDR2 and CDR3, respectively.

Figure 2 shows the amino acid (AA) sequence design of CDR-Grafted anti-RSV F Protein V_L. The figure depicts the AA sequence for the human K102 V_L (SEQ ID NO:19) before grafting, CDR grafted V_L, (SEQ ID NO:20) and murine MAb1308F V_L (SEQ ID NO:21) from which the CDR sequence was grafted. The heavily underlined regions identify the CDR sequence which was grafted into the human K102 V_L and each of the three regions is identified as CDR1, CDR2 and CDR3, respectively.

Figure 3 depicts the oligonucleotides used to make Hu1308V_H, the sequences which are underlined are the specific primer sequences. Ins B1

Figure 4 depicts the oligonucleotides used to make Hu1308V_L, the sequences which are underlined are the specific primer sequences. Ins B2

Figure 5 depicts the plasmid construction of the expression vectors for Humanized 1308.

Figure 6 depicts a graph of the Neutraliziation of RSV as percent neutralization versus ng MAb per reaction for neutralizing with Cos Hu1308F and with Mu1308F.

Figure 7 shows the amino acid (AA) sequence design of CDR-Grafted anti-RSV F glycoprotein V_H. The figure depicts the AA sequence for the human COR V_H (SEQ ID NO:30) before grafting, CDR grafted V_H, (SEQ ID NO:31) and murine MAb1129 V_H (SEQ ID NO:32) from which the CDR sequence was grafted. The heavily underlined regions identify the CDR sequence which was grafted into the human COR V_H and each of the three regions is identified as CDR1, CDR2 and CDR3, respectively.

Figure 8 shows the amino acid (AA) sequence design of CDR-Grafted anti-RSV F Protein V_L. The figure depicts the AA sequence for the human K102 V_L (SEQ ID NO:33) before grafting, CDR grafted V_L, (SEQ ID NO:34) and murine MAb1129 V_L (SEQ ID NO:35) from which the CDR sequence was grafted. The heavily underlined regions identify the CDR sequence which was grafted into the human K102 V_L and each of the thr regions is identifi d as CDR1, CDR2 and CDR3, respectively.

Figure 9 shows the oligonucleotides used to construct the humanized 1129 VH.

Figur 10 shows binding data for humanized 1129 in an ELISA assay.

DETAILED DESCRIPTION OF THE INVENTION

Applicants have found that transplantation into a human antibody, of only the genetic information for at least one CDR from each of the variable heavy and variable light chain derived from murine monoclonal antibody against RSV antigen, is effective for the prevention and treatment of RSV in animals. Preferably the murine antibody is a neutralizing antibody against RSV. Another aspect of the present invention provides for the murine antibody to be an antibody against RSV F antigen. Preferably, the murine antibody is neutralizing antibody against RSV F antigen. The substitution of the mouse CDR's into the human variable framework segments minimizes the potential for human anti-mouse antibody (HAMA) responses while retaining binding affinity and specificity for antigen, RSV F protein. Since, the CDR's do not contain characteristic murine or human motifs, the human antibodies containing the murine antibody CDR's are essentially indistinguishable from completely human antibodies, thereby, minimizing the human antibody response while retaining binding affinity and specificity for RSV F antigen.

The development of a humanized antibody against RSV F antigen began with a murine antibody against RSV F antigen. Examples of murine antibodies of this type are: MAb 1436C, MAb 113, MAb 112, MAb 151, MAb 1200, MAb 1214, MAb 1237, MAb 1129, MAb 1121, MAb 1107, MAb 131-1, MAb 43-1, MAb 1112, MAb 1269, MAb 1243, MAb 1331H, MAb 1308F and MAb 1302A (see citation 21).

An aspect of the present invention provides that the CDRs of the human antibody are comprised of three complementarity determining regions (CDRs) from each variable heavy and variable light chain of th murin antibody.

The murine antibodies against RSV F antigen have been mapped by competitive binding and reactivity profiles of virus escape mutants to three broad antigenic sites (A, B, C) containing 16 distinct epitopes (20). The epitopes within antigenic sites A and C have shown the least variability in natural isolates.

Therefore, another aspect of this invention provides for a human antibody containing at least one CDR from each variable heavy and variable light chain of at least one murine antibody against RSV F antigen which is specific for antigenic site A or C. In one aspect, this invention provides for the murine antibody against RSV F antigen specific for antigenic site C, where the murine antibody is MAb 1308F.

In such an embodiment of this invention a human antibody contains CDR's of the variable heavy chain of murine antibody MAb 1308F against the RSV F antigen. The CDR variable heavy chain of MAb 1308F comprises three CDRs having the following amino acid sequences: Nos. 31 to 35, 47 to 60 and 99 to 106. In addition, this embodiment contains CDR's of a variable light chain of MAb 1308F of murine antibody against RSV F antigen. The CDR variable light chain comprises three CDR's having the following amino acid sequences: Nos. 24 to 34, 50 to 56 and 89 to 97.

Another aspect of this invention provides for a human antibody containing at least one CDR from each variable heavy and variable light chain of at least one murine antibody against RSV F antigen which is specific for antigenic site C. Preferably, this invention provides for the murine antibody against RSV F antigen specific for antigenic site C, where the murine antibody is MAb 1129.

In the embodiment of this invention a human antibody which contains CDR's of the variable heavy chain of murine antibody MAb 1129 against the RSV F antigen. The CDR variable heavy chain of MAb 1129 comprises three CDRs having the following amino acid sequences: Nos. 31 to 36, 52 to 67 and 100 to 109. In addition, this embodiment contains CDR's of a variable light chain of MAb 1129 of murin antibody against RSV F antigen. The CDR variabl

light chain comprises three CDR's having the following amino acid sequences: Nos. 24 to 33, 51 to 56 and 89 to 96.

An additional aspect of applicants' invention is a process for preventing or treating RSV infection comprising administering to the animal an effective amount of a human antibody containing at least one CDR from each variable heavy and variable light chain, of at least one murine antibody against RSV F antigen.

Another aspect of applicants' invention is a composition comprising administering an effective amount of the human antibody as described above in conjunction with an acceptable pharmaceutical carrier. Acceptable pharmaceutical carriers include but are not limited to non-toxic buffers, fillers, isotonic solutions, etc.

The composition of Applicant's invention may be administered topically or systemically. Examples of topical administration are intranasal administration and inhalation of an aerosol containing the human antibody composition. Systemic administration may be accomplished by intravenous or intramuscular injection of the human antibody composition.

A preferred aspect of Applicants' invention is that the human antibody is administered as part of a plurality of human antibodies against RSV F antigen. These antibodies can be against the same or different epitopes of the RSV F antigen.

Additionally, the human antibody of this invention can be used clinically for diagnosing respiratory syncytial virus in patients. Because of their affinity for RSV F antigen these human antibodies can be used in known diagnostic assay procedures for detecting the presence and concentration of RSV F antigen cells in samples, e.g., body fluids. The human antibodies of the present invention can for example be attached or bound to a solid support, such as latex beads, a column, etc., which are then contacted with a sample believed to contain RSV F antigen.

Applicants' development of human antibodies against RSV, began with murine hybridoma cells producing murine monoclonal antibodies

which have been shown to neutralize RSV in vitro and protect cotton rats against lower r spiratory tract infection with RSV.

One such antibody was selected, which is specific for antigenic site C, to produce mouse-human chimeric antibodies. This antibody was chosen on the basis that it: (i) reacted with a large number of virus strains tested (at least 13 out of 14 isolated); (ii) retained neutralizing activity against virus escape mutants selected with other anti-F antibodies and (iii) blocked RSV replication when administered at low doses to cotton rats by intranasal route prior to virus challenge. The antibody showed significant reduction in pulmonary virus titer among antibodies in that respective region. Murine antibody 1308F, specific for the C region of RSV F protein, was chosen as the initial target for humanization.

In summary, the human antibodies were constructed as follows: the RNA was extracted from the murine antibody-producing cell line, the murine variable regions which are responsible for the binding of the antibody to RSV were cloned and sequenced, resulting in the identification of the murine antibody CDRs. Then a human variable heavy and light chain framework sequence having the highest homology with the variable heavy and light chain murine antibody, was selected. A human framework sequence such as described above is best able to accept the murine-derived CDRs.

The murine 1308F variable heavy chain was compared to various human germline genes, the highest homology was to the human germline gene HV3. The two sequences were 62% homologous overall and 65% in the framework regions. Significantly, there is good homology at the junctions of the CDR segments and the frameworks with the exception of the 5' end of FR2. The murine derived variable heavy chain CDRs were then substituted into the variable heavy chain human germline gene HV3. The mouse and human sequences as well as that of a potential CDR-Grafted combination of the two is shown in Figure 1.

A similar analysis of the V_L region revealed high homology to the human germ line V-Kappa gene K 102. The alignment of these sequences is shown in Figure 2. In this case the homology is 62% overall and 73% in the framework regions. The murine-derived variable light CDRs were then substituted into the human variable light chain of human germline gene K102.In each case a human J-region can be selected which is identical to the mouse sequence.

In another embodiment, murine 1129 variable heavy chain was compared to various human variable region amino acid sequences, the highest homology was to the human rearranged COR sequence. The two amino acid sequences were 75% homologous overall and 80% in the framework regions. Significantly, there is good homology at the junctions of the CDR segments and the frameworks. The murine derived variable heavy chain CDRs were then substituted into the variable heavy chain human COR V_H sequence. The mouse and human sequences as well as that of a potential CDR-Grafted combination of the two is shown in Figure 1.

A similar analysis of the V_L region revealed high homology to the human germ line K102. The alignment of these sequences is shown in Figure 8. In this case the homology is 73% overall and 82% in the framework regions. The murine-derived variable light CDRs were then substituted into the human variable light chain of human germline K102. In this case a human J-region, human JK4, was selected which is similar to the mouse sequence.

Therefore, human antibodies are expressed and characterized relative to the parental murine antibodies to be certain that the genetic manipulation has not drastically altered the binding properties of the antibodies.

Applicants present herein examples which are further illustrative of the claimed invention but not intended to limit the invention.

Examples 1

cDNA cloning and sequencing of anti-RSV F Protein antibody 1308F

cDNA copies of the V_H and V_L of the target antibody were generated as follows. The first strand CDNA r action was carried out using AMV reverse trenscriptase and a phosphorylated oligonucleotide primer complementary to a segment of the mRNA coding for the constant region of the particular heavy or light chain isotype. For 1308F the isotype is gammal, kappa and the specific oligonucleotides were 5'AGCGGATCCAGGGGCCAGTGGATAGAC (SEQ ID NO:1) complementary to codons 129-137 of the CH1 region of the murine Gammal gene, and 5'TGGATGGTGGGAAGATG (SEQ ID NO:2) complementary to codons 116-122 of the murine C-kappa gene. The primer anneals to a segment of the mRNA adjacent to the variable region. Second strand cDNA synthesis was carried out using RNase H and E. coli DNA polymerase I, as described by Gubler and Hoffman (Gene 25,;263, 1983), followed by T4 DNA polymerase to assure that blunt ends are produced.

Signal	V	J	C	mRNA
	1st strand cDNA			
	2nd strand cDNA			

The ds-cDNA was ligated into pUC18 which had been digested with restriction endonuclease SmaI and treated with alkaline phosphatase. The ligation was used to transform E. coli DH5a by the method of Hanahan (J. Mol. Biol. 166;557, 1983). Oligonucleotide probes corresponding to C-region sequence lying between the first strand cDNA primer and the V-region were used in colony hybridizations to identify transformants carrying the desired cDNA segment. The specific probe sequences were, GGCCAGTGGATAGAC (SEQ ID NO:3) complementary to codons 121-125 of murine CH1 regions and TACAGTTGGTGCAGCA (SEQ ID NO:4) complementary to codons 110-115 of c-Kappa, respectively. Candidate plasmids, isolated from colonies which were positive in the hybridization, were analyzed by

digestion with restriction endonucleases Eco RI and Hind III to release th cDNA insert. Those with inserts of 400-500bp were subjected to DNA sequencing.

The cDNA inserts were inserted into M13 mp18 and mp19 for the determination of the DNA sequence on both strands. Single stranded DNA from the resulting recombinant bacteriophage was isolated and sequenced by the dideoxy chain termination method (Proc. Nat. Acad. Sci. USA 74; 5463, 1977).

In order to confirm that the pair of rearranged and somatically mutated V gene cDNA's isolated from the 1308F hybridoma represented those which were in the 1308F antibody, a single-chain Fv gene was generated, expressed in and secreted from mammalian cells, then assayed for binding to RS virus. Competition binding experiments then were used to demonstrate the identity of the binding site.

Example 2

Design and assembly of human 1308F V_H and V_L

The CDR regions of the V_H and V_L were identified by comparing the amino acid sequence to known sequences as described by Kabat (38). In order to select the human framework sequences best able to accept the mouse derived CDR sequences in a conformation which retains the structure of the antigen combining site, the following strategy was employed. First, the sequence of the murine V_H and V_L regions will be compared to known human sequences from both the Genbank and NBRF protein databanks using the Wordsearch program in the Wisconsin package of sequence manipulation programs (Nucleic Acid Res. 12;387). The best several human V-regions were then analyzed further on the basis of similarity in the framework regions, especially at the junctions of the framework and CDR regions (see Figures 1 and 2).

The CDR-grafted V_H region together with the respective leader sequ nce of the human v-region gene was synthesized d novo using four overlapping oligonucleotid s ranging from 100-137 nucleotides

in length (see Figure 3). The oligonucleotides were first allowed to anneal in pairwise combinations and extended with DNA polymerase to generate approximately 200bp ds DNA fragments with an overlapping region. the fragments were then mixed and subjected to PCR using primers at the 3'end of one fragment and the 5' end of the other fragment. The only product which can be formed under these condition is the full length V_H segment. The specific primer sequences are underlined in Figure 3. An endonuclease <u>Sac I</u> site was included at the 3' end of the V_H sequence in order to join it to a human constant region gene segment.

The CDR-grafted V_L region was synthesized in a similar way (see Figure 4). In this instance the initial 200bp fragments were amplified separately and inserted into separate plasmeds. The fragment coding for the amino terminus was cloned into a pUC18 derivative as an NcoI-SmaI fragment while the fragment coding for the carboxyl-terminus was cloned as a SmaI to Hind III fragment. The fragments were subsequently combined via a SmaI site at the junction. The oligonucleotides are indicated in Figure 4. A Hind III site was included near the 3' end of the gene segment in order to join it to a human C-kappa gene.

<u>Example 3</u>

<u>Construction of Vectors for 1308F expression</u>

The NcoI-SacI fragment representing the humanized V_H was joined to a SacI -Notl fragment representing a human c-Gamma I CDNA and inserted into pS 18 (which is pUC 1 8 with Ncol and NotI restriction sites incorporated into the polylinker region between the BamHI and Kpnl sites). The humanized 1308F-gammal gene on a SacI-NotI fragment was then combined with a Pvul-NotI fragment from pSJ37 carrying a poly A addition site and a PvuI-SacI fragment from pSV2-dhfr-pCMV containing the SV40 origin of replication, a dhfr gene and the CMV imm diate early promoter. Th resulting plasmid was designated pSJ60.

The NcoI-HindIII fragment representing the humanized V_L was joined to a HindIII-Notl fragment representing a human c-Kappa CDNA in pS18. The humanized 1308F-Kappa gene on a SalI-NotI fragment was then combined with a Pvul-NotI fragment from pSJ37 carrying a poly A addition site and a PvuI-SalI fragment from pSV2-dhfr-pCMV, containing the SV40 origin of replication, a dhfr gene and the CMV immediate early promoter. The resulting plasmid was designated pSJ61.

Finally pSJ60 and pSJ61 were combined into a single plasmid containing both the light and heavy chains and expression signals. This was accomplished by isolating a PvuI-Bam HI fragment from pSJ61 carrying the light chain with a Pvu I - Bgl II fragment from pSJ60 carrying the heavy chain to generate pSJ66. (See Figure 5).

Example 4

Transfection of Cosl cells with PSJ60 and PSJ61

Transfections were carried out according to the method of McCutchan and Pagano (J. Nat. Can. Inst. 41: 351-356, 1968) with the following modifications. COS 1 cells (ATCC CRL1650) were maintained in a humidified 5% C02 incubator in 75 cm^2 tissue culture flasks in Dulbecco's Modified Eagle Medium (DMEM, GIBCO #320-1965) supplemented with 10% Fetal Bovine Serum (FBS, GIBCO #200-6140) and 2mM L-glutamine (BRL #320-5030) and passed at a split ratio of 1:20 when the cells had reached confluence. 48 hours prior to transfection, 5 100mm tissue culture dishes were seeded with 1.5 x 10^6 cells per dish in 12ml DMEM, 10% FBS, 2mM L-glutamine, 1% penicillin-streptomycin (P-S, GIBCO #600-5070). The day of the transfection, 120 ug each of the plasmids pSJ60 and pSJ61 were combined, ethanol precipitated, and aseptically resuspended in 2.5ml Tris-Buffered-Saline. The resuspended DNA was added dropwise, with mixing, to 10ml of DMLEM containing 1 mg/ml DEAE-dextran (Phamiacia #17-0350-01) and 250 uM chloroquine (Sigma #C6628). The medium was removed from th COS1 c lls in the 100 mm dishes and the c lls wer wash d once with Dulb cco's phosphate

buffered saline (D-PBS, GIBCO #310-4190), and 2.5ml DMEM supplemented with 10% NuSerum (Collaborative Research #55000) w re added to each plate. 2.5ml of the DNA/DEAE-dextran/chloroquine mix were added dropwise to each plate, the plates swirled to mix the DNA, and were returned to the incubator. After 4 hours in the incubator, the supernatant was aspirated from the cells and the cells were washed once with 5ml D-PBS. The cells were shocked for 3 minutes by the addition of 5ml of 10% dimethylsulfoxide (DMSO) in D-PBS at room temperature. The DMSO was aspirated from the cells and the cells were washed with 5ml D-PBS. 14ml of DMEM/10% FBS/2mM L-glutamine/1%P-S were added to each plate and the plates were returned to the incubator.

Three days post-transfection the medium was removed from the plates, pooled, and stored at -20°C. The cells were harvested, pooled, and seeded into 4 150cm^2 tissue culture flasks two with 40ml DMEM/10% NuSerum and two with 40ml DMEM/10% FBS/2mM L-glutamine. The medium was collected and the cells refed at 7, 10, and 14 days. In this way a total of 125ug of humanized 1308F antibody was accumulated in 310ml of medium supplemented with FBS and 85ug in 240ml of medium supplemented with NuSerum.

Example 5

Transfections of COS 1 cells with PSJ66

48 hours prior to transfection, 5 100mm tissue culture dishes were seeded with 1.5 x 10^6 cells per dish in 12ml DMEM, 10% FBS, 2mM L-glutamine, 1% penicillin-streptomycin (P-S, GIBCO #600-5070). The day of the transfection, 125ug of the plasmid pSJ66 were ethanol precipitated and aseptically resuspended in 1.0 ml Tris-Buffered-Saline. The resuspended DNA was added dropwise, with mixing, to 4.0ml of DMEM containing 1mg/ml DEAE-dextran (Pharmacia #17-0350-01) and 250uM chloroquine (Sigma #C6628). The medium was removed from the COS1 cells in the 100mm dishes and the cells were washed once with Dulbecco's phosphate buff red saline (D-PBS, GIBCO #310-4190), and 2.5ml DMEM suppl ment d with 10% NuSerum

(Collaborative Research #55000) were added to each plate. 2.5ml of the DNA/DEAE-dextran/chloroquine mix were added dropwise to each plate, the plates swirled to mix the DNA, and were returned to the incubator. After 4 hours in the incubator, the supernatant was aspirated from the cells and the cells were washed once with 5ml D-PBS. The cells were shocked for 3 minutes by the addition of 5ml of 10% dimethylsulfoxide (DMSO) in D-PBS at room temperature. The DMSO was aspirated from the cells and the cells were washed with 5ml D-PBS. 14ml of DMEM/10% FBS/2mM L-glutamine/1%P-S were added to each plate and the plates were returned to the incubator.

Three days post-transfection the medium was removed from the plates, pooled, and stored at -20°C. The cells were harvested, pooled, and seeded into 4 150cm^2 tissue culture flasks two with 40 ml DMEM10% NuSerum and two with 40 ml DMEM10% FBS/2mM L-glutamine. The medium was collected and the cells refed at 7, 10, and 14 days. In this way a total of 190ug of humanized 1308F antibody was accumulated in 310ml of medium supplemented with FBS and 120ug in 240ml of medium supplemented with NuSerum.

The concentration of humanized 1308F antibody secreted from the Cos1 cells into the medium was determined using a capture ELISA. Goat anti-human IgG Fc coated onto 96 well plates was used to capture the humanized antibody. Peroxidase conjugated goat anti-human whole IgG developed with a chromogenic substrate was then used to detect the bound antibody. A purified human IgG1/Kappa preparation was used to calibrate the assay.

<u>Example 6</u>

<u>Neutralization of RSV with humanized 1308F</u>

METHODS:

RSV was neutralized with either humanized 1308F from Cos cell supernatant or purified 1308F murine monoclonal antibody. This was done by incubating 50 plaque-forming units of RSV with serial 2-fold dilutions of antibody for 1.0 hour at 37°C. Confluent monolay rs of Hep2 cells in 24 well panels were infected with 100μl

of antibody treated virus, untreated control virus, and mock infected controls. Incubated for 1.5 hours at 37°C, humidified , and 5% CO_2 and overlayed with 1.5mL EMEM, 1% FBS, and 1% methyl cellulose. Cells were fixed and stained with glutaldehyde and crystal violet on day 4. Plaques were counted in triplicate wells and plotted as percent neutralization. The results shown in Figure 6 indicate that both the purified murine 1308F monoclonal and the humanized 1308F monoclonal antibody at 5 to 10 ng per well yield similar 50% reductions in RSV plaques.

Example 7

Generation of a CDR-grafted A-site antibody 1129

Poly-A+ RNA was purified from a lysate of 2 x 107 murine 1129 hybridoma cells using oligo-dt cellulose. First strand CDNA was made from 1 ug pA+ RNA using random hexamer primers and AMV reverse transcriptase" 1ug pA+ RNA, 50mM Tris-HCl pH 8.5, 8mM Mg_2Cl, 30mM KCl, 1 mM dithiothrietol, 1 mM dNTP's, 25 units of placental ribonuclease inhibitor, 33uM random hexamer and 10 units of AMV reverse transcriptase for one hour at 42°C. The cDNA from the 1129 VL region was amplified by PCR using oligonucleotides SJ41 and SJ11, see Table 1. cDNA from the 1129 VH region was similarly amplified using oligonucleotides SJ42 and SJ10, see Table 1.

TABLE 1

SJ10
AGCGGATCCAGGGGCCAGTGGATAGAC (SEQ ID NO:1)

SJ11
GATGGATCCAGTTGGTGCAGCATC (SEQ ID NO:5)

SJ41
CACGTCGACATTCAGCTGACCCAGTCTCCA (SEQ ID NO:6)

SJ42
CGGAATTCAGGTIIAICTGCAGIAGTC(A,T)GG (SEQ ID NO:7)
{I = deoxy-Inosine}

SJ53
CCCAAGCTTGGTCCCCCCTCCGAACGTG (SEQ ID NO:8)

SJ154
B GGCGTCGACTCACCATGGACATGAGGGTCC(C/T)CGCTCAGC (SEQ ID NO:9)

~~SJ155 (H1129L CDR 1)
GTCACCATCACTTGCAAGTGCCAGCTGAGTGTAGGTTACATGCACTGGTACC
AGCAG~~

SUB E1

~~SJ157 (H1129L CDR 3)
GCAACTTATTACTGCTTTCAGGGGAGTGGGTACCCATTCACGTTCGGAGGGG
GG~~

~~SJ168
GTGACCAACATGGACCCTGCTGATACTGCCAC~~

~~SJ169
CCATGTTGGTCACTTTAAGGACCACCTGG~~

~~SJ170
CCAGTTTACTAGTGTCATAGATCAGGAGCTTAGGGGC~~

~~SJ171
TGACACTAGTAAACTGGCTTCTGGGGTCCCATCAAGG~~

~~PCR conditions~~

~~0.5uL of 1st strand cDNA, 10mM Tris-HCl pH8.3, 50mM KCl, 1.5mM Mg2Cl, 0.2mM dNTP's, 0.001 % gelatin, 1 uM each primer, 1 ng DNA template and 2.5u AmpliTaq(TM) DNA polymerase (Perkin Elmer - Cetus). 94° 1 minute, 55° 2 minutes, 72° 2 minutes in Perkin Elmer 480 thermocycler for 25 cycles. The resulting DNA fragment(s) were then extracted once with phenol/chloroform (1/1), precipitated with 2.5 volumes of ETOH, resuspended in the appropriate restriction endonuclease buffer and digested with restriction endonucleases to produce cohesive ends for cloning. The resulting fragments were then separated by electrophoresis on a 1 % agarose gel. After staining the gel with ethidium bromide the fragments were excised and purified from the agarose by freezing and extraction in the presence of phenol.~~

~~The fragments were then digested with restriction endonucleases EcoR1 and BamH1 and clon d into plasmid pUC18. The ins rts were~~

then sequenced by th dideoxynucleotide chain termination method using modified T7 DNA polymerase (Seqeunase, US Biochemical). The translated sequences were compared to human antibody protein sequences. The VL was found to be most homologous to the K102 light chain and the VH was found to be most homologous to the Cor VH region. The 1129 Fv region was then modeled by substitution of the residues from the 1129 VL and VH sequence into the coordinates of corresponding residues in the crystal structure the MCPC603 antibody. Residues were identified as being integral to the folded structure or solvent exposed by visual inspection of the model.

Several residues which were integral and which were different in the mouse and human sequences were left as the mouse residue in order to maintain the integrity of the Fv and thus the binding site. Such residues were 31,83,113, and 116 on the VH and 47 in the VL region. The resulting sequences are shown in figures 7 and 8.

The designed humanized 1129 VH was constructed using synthetic INS B oligonucleotides SJ147-SJ153 (Figure 9) which were combined using PCR. The products of this PCR were B3 then digested with Ncol and Sacl and cloned into pladmid vector pSJ40 which is a pUC18 derivative in which an out of frame lacZ1 segment is restored in frame as a fusion to an in-frame V region segment when such a segment is inserted as an Ncol-Sacl fragment. A plasmid containing an insert in which 5 mutations were clustered in a single 50 bp region was then subjected to repair of these changes using recombinant PCR and the primers SJ168 and SJ169, see Table 1.

The VL was generated by site directed mutagenesis of the humanized 1308F light chain gene. Oligonucleotides SJ155, see Table 1, (CDR1), and SJ157 (CDR3) were used to separately mutagenize the H1308L gene. Mutagenesis was carried out using T7 DNA polymerase on uracil containing single strand d DNA templat s g nerated in E.

coli strain BW313 (dut-,ung-) and subsequently transformed into E. coli strain DH5 (dut+,ung+). The two mutants were combined and CDR2 introduced by recombinant PCR using oligonucleotides SJ170, SJ154, see Table 1, (5'end) and SJ171, SJ53, see Table 1, (3'end). The CDR-grafted VH and VL genes were placed into pSJ60 (see Example 3) and pSJ61 (see Example 3), respectively as Ncol-Sacl fragments in place of the H1308F Vregion segments resulting in plasmids pSJ81 and pSJ105. In addition the murine VH and VL cDNA segments were similarly joined to human C-Gamma1 and CKappa respectively to generate expression vectors pSJ75 and pSJ84.

Example 8

Hu1129 Transient Expression

COS1 cells (ATCC CRL1650) were maintained in a humidified 5% CO_2 incubator in 75 CM^2 tissue culture flasks in Dulbecco's Modified Eagle Medium (DMEM, GIBCO #320-1965) supplemented with 10% fetal bovine serum (FBS, GIBCO #200-6140) and 2mM L-glutamine (GIBCO #320-5030) and passed at a split ratio of 1:20 just prior to reaching confluence.

Transfections were carried out according to the method of McCutchan and Pagano (J. Nat. Can. Inst. 41: 351-356, 1968) with the following modifications. Twenty four hours prior to transfection 100 mm tissue culture dishes (Corning # 25020) were seeded with 2 x 106 COS1 cells per dish in 14 ml DMEM, 10% FBS, 2mM L-glutamine. The day of the transfection 10 ug of the Hu1129 heavy chain plasmid (pSJ81, from Example 7 were combined with 10 ug of the Hu1129 kappa light chain plasmid pSJ105, from Example 7, the DNA was ethanol precipitated and aseptically resuspended in 1.0 ml Tris-Buffered-Saline. The resuspended DNA was added dropwise, with mixing, to 4.0 ml of DMEM containing 1 mg/ml DEAE-dextran (Pharmacia #170350-01) and 250 uM Chloroquine (Sigma #C6628). Th m dium was removed from the COS1 c ll dish s, the cell monolayers w re washed once with 10 ml Dulbecco's phosphate buffered salin

(D-PBS, GIBCO #310-4190), and 2.5 ml DMEM supplem nt d with 10% NuSerum (Collaborative Research #55000) and 2mM L-glutamine were added to each plate. 2.5 ml of the DNA/DEAEdextran/chloroquine mix were added dropwise to each plate, the plates were swirled to mix the DNA, and returned to the incubator. After an eight hour DNA adsorption period the plates were removed from the incubator and the supernatant was aspirated from the plates. The cells were shocked by the addition of 5 ml of 10% DMSO in D-PBS per plate for 3 minutes at room temperature, after which the DMSO was aspirated from the cells and the cells were washed once with 5 ml D-PBS. 15 ml DMEM, 10% NuSerum, 2mM L-glutamine (production medium) were added to each plate and the plates were returned to the incubator.

Seventy two hours post-transfection the conditioned medium was harvested from the plates and stored at -20°C, andl 5 ml production medium was added to the plates and the plates were returned to the incubator. Ninety six hours later the medium was collected from the plates and stored at 20°C.

Example 9

Quantitation of Hu1129

Quantitation of the Hu1129 IgG1 antibody secreted into the medium by the COS1 cells was performed using a sandwich type ELISA. In brief, Nunc Maxisorp Immunoplates (Nunc #439454) were coated with 50 ul/well of 0.5 ug/ml goat anti-human IgG Fc (Cappel #55071) in 0.1 M sodium bicarbonate pH 9.6 for 3 hours at room temperature. The wells were washed three times with 0.01 M sodium phosphate pH 7.4, 0.15 M NaCl, 0.1 % Tween 20 (PBS-T). Nonspecific protein binding to the plate was blocked by treatment of the wells with 200 ul/well of 3% (w/v) nonfat dry milk in PBS for 30 minutes at room temperature. A purified human IgG1 kappa standard (Sigma #1-3889) was made up at 100 ng/ml in PBS-T and serially diluted 1:2 to 1.56 ng/ml, and 50 ul of each were added to duplicate wells of the assay plat . COS1 c ll sup rnatants were diluted in PBS-T and duplicate

50 ul samples were added to the plate. After an one hour room temperature incubation the w lls were evacuated and washed three times with PBS-T. To detect the presence of bound Hul 129 antibody, horseradish peroxidase conjugated affinity purified goat anti-human IgG (whole molecule, Cappel #3601-0081) was diluted 1:1 000 in PBS-T and 50 ul was added to each well of the assay plate and incubated at room temperature for one hour. The plate was washed three times with PBS-T and 100 ul of the chromogenic substrate TMBlue (TSI #TM102) was added to each well. The plate was incubated at room temperature in the dark for ten minutes and the reaction was stopped by the addition of 50 ul per well of 4.5 M H_2SO_4. The plate was read at 450 nm using a Molecular Devices Vmax microplate reader, and data analysis was performed using Softmax software (Molecular Devices) running on an IBM P/S2 model 80 computer.

During the first seventy two hours of production the COS1 cells produced 0.06ug/ml Hu1129, for a total of 0.9ug. In the next ninety six hours of production the COS1 cells produced 0.99ug/ml Hu1129, for a total of 14.85ug.

Example 10

Hu1129 Binding Assay

Binding assays of the Hu1129 were performed in a capture ELISA, essentially as for the quantitation ELISA, but with the following changes. Plates were coated with the Mul 331 antibody at 0.5ug/well, the wells were blocked with 3% non-fat milk in PBS-T, and 50ul of RSV infected HEP2 cell lysate was added to each well and incubated at room temperature for 1 hour. The remainder of the assay was carried out as for the quantitation assay starting with the addition of diluted samples to the wells. Results were analyzed as a double reciprocal plot of OD vs antibody conc ntration from which an apparent Kd for the H1129 molecule of

0.7nM was determined compared to 10nM for the M1129HuGamma1,Kappa antibody.

RSV neutralization assays on H1129 and ch1129 antibody were performed according to the following procedure:

1. Unwrap 96 well Costar cell culture plates in hood.

2. Warm Growth Medium (GM) to 37 C.

3. Thaw MA104 cells at 37 C. Dilute to ~150,000 cells per mL with GM. Mix cells and dispense 200 μl per well.

4. Culture cells 37 C, 5% CO_2, and humidified overnight before infection.

5. Dilute RSV Stock to 10,000 pfu per mL in Maintenance Medium (MM).

6. Mix equal volume of Antibody diluted in MM with equal volume of diluted RSV. Incubate at 37 C, 5% CO_2, and humidified for 1.0 h before infection.

7. Infect replicate wells of MA104 cells with 200 μl of the Antibody and Virus mixture. Infect replicate wells with virus and mock infected controls.

8. Wrap the plates in cellophane and incubate at 37 C, 95% humidity, and 5% CO_2 for 5 days.

9. <u>ELISA for RSV:</u> Aspirate each well; add 100 μl 80% Acetone/PBS (vol./vol.) and incubate at room temperature 30 minutes.

10. Aspirate each well and air dry for 30 minutes on the grill of a laminar flow hood.

11. Wash 4 times with PBS, 0.05%Tween 20.

12. Add 100 μl of monoclonal antibody to RSV F-protein to each well. Incubate for 1.0 h at 37 C.

13. Wash 4 times with PBS, 0.05%Tween 20.

14. Add 100 μl of anti-murine antibody goat serum-horse radish peroxidaze conjugate to each well. Incubate for 1.0 h at 37 C.

15. Wash 4 times with PBS, 0.05%Tween 20.

16. Add 100 μl of a freshly prepared 1:1 mixture of ABTS and peroxide to each well. Incubate at room temperature until the optical density (405 nm) of the virus control is 5 to 10 times that of the mock infected controls.

Appendix:

<u>Growth Medium (GM)</u>: Minimum Essential Medium (Eagle) with
Earle's BSS,
2mM glutamine,
Eagle's non-essential amino acids 0.1 mM final,
Fetal bovine serum 10% (v/v),
Penicillin 50 units/ml,
Streptomycin 50 mcg/ml

<u>Maintenance Medium (MM):</u> as above with serum reduced to 1 to 2%.

MA104 cell stocks are grown up in T150 flasks with Growth Medium. Stocks are frozen at 3 x 10^6 cells per 1.8 mL vial in 10% DMSO and Growth Medium. Stored in a LN_2 refrigerator.

RSV stocks: are grown up in MA104 (monkey kidney) or Hep 2 cells in T150 flasks. Add ~0.2ml (~100,000 pfu) virus stock per confluent T150. Adsorption for 1.0 h at room temperature. Then add 20 mL maintenance medium with 1% fetal bovine serum. Incubate 4-5 days at 37 C. Collect cells just before 100% cpe by scraping. Spin down cells; remove all but 10 mL of supernatant. Freeze (dry ice-ethanol bath) thaw cell pellet, vortex, re-freeze, and store virus stock in LN2 refrigerator.

ELISA Antibody Buffer: PBS, 0.05%Tween 20 (w/v), 2.0% goat serum (v/v) and 0.5 % gelatin (w/v).

RSV F Protein Antibody: Chemicon Mab 858-1 anti-RSV fusion protein diluted ~1: 5000 in ELISA Antibody Buffer.

Anti-Murine Serum.: Fisher horse radish peroxidase conjugated to goat anti-mouse IgG (Heavy Chain Specific) diluted ~1: 4000 in ELISA Antibody Buffer.

The results are shown in Figure 10, and indicate 25ng/mi achieved 50% neutralization in this assay while 45ug/ml of the ch1129 antibody was required for 50% neutralization in this experiment. Over a series of 6 separate assays the mean 50% neutralization value for H1129 was 17ng/ml. As a control and to compare potency we also assayed a polyclonal human IgG preparation made from the plasma of individuals with high neutralizing titers for RSV. This preparation, termed RSVig (lot#4), gave a mean 50% neutralization value of 2.3ug/ml over 3 experiments. Thus the H1129 is 100-fold more potent in this assay as the enriched polyclonal pr paration.

Example 11

Kin tic Analysis of Humanized RSV Mabs by BIAcoreTM

The kinetics of interaction between humanized RSV Mabs and the RSV F protein was studied by surface plasmon resonance using a Pharmacia BIAcoreTM biosensor. A recombinant baculovirus expressing a C-terminal truncated F protein provided an abundant source of antigen for kinetic studies. The supernatant, which contained the secreted F protein, was enriched approximately 20-fold by successive chromatography on concanalvalin A and Q-sepharose columns. The pooled fractions were dialyzed against 10 mM sodium citrate (pH 5.5), and concentrated to approximately 0.1 mg/ml. An aliquot of the F-protein (100 ml) was amine-coupled to the BIAcore sensor chip. The amount immobilized gave approximately 2000 response units (Rmax) Of signal when saturated with either H1129 or H1308F. This indicated that there was an equal number of "A" and "C" antigenic sites on the F-protein preparation following the coupling procedure. Two unrelated irrelevant Mabs (RVFV 4D4 and CMV H758) showed no interation with the immobolized F protein. A typical kinetic study involved the injection of 35 ml of Mab at varying concentrations (25-300 nM) in PBS buffer containing 0.05% Tween-20 (PBS/Tween). The flow rate was maintained at 5 ml/min, giving a 7 min binding phase. Following the injection of Mab, the flow was exchanged with PBS/Tween buffer for 30 min for determining the rate of dissociation. The sensor chip was regenerated between cycles with a 2 min pulse of 10 mM HCl. The regeneration step caused a minimal loss of binding capacity of the immobilized F-protein (4% loss per cycle). This small decrease did not change the calculated values of the rate constants for binding and dissociation.

The affinity of the various Mabs for binding to the F protein was calculated from the ratio of the first order rate constant for dissociation to the second order rat constant for binding (K_d =

k_{diss}/k_{assoc}). The value for k_{assoc} was calculated based on the following rate equation:

(1) $$dR/dt = k_{assoc}[Mab]R_{max} - (k_{assoc}[Mab] + k_{diss})R$$

where R and Rmax are the response units at time t and infinity, respectively. A plot of dr/dt as a function of R gives a slope of (k_{assoc}[Mab] + k_{diss})- Since these slopes are linearly related to the [Mab], the value k_{assoc} can be derived from a replot of the slopes versus [Mab]. The slope of the new line is equal to **kassoc**. Although the value of **kdiss** can be extrapolated from the Y-intercept, a more accurate value was determined by direct measurement of k_{diss}. Following the injection phase of the Mab, PBS/Tween buffer flows across the sensor chip. From this point, [Mab] = 0. Equation (1) thus reduces to:

(2) $$dr/dt = k_{dissr} \text{ or } dR/R = k_{diss}dt$$

Integration of equation (2) gives:

(3) $$\ln(R_0/R_t) = k_{diss}t$$

where R_0/R_t) are the response units at time 0 (start of dissociation phase) and t, respectively. Lastly, plotting $In(R_0/R_t)$ as a function of t gives a slope of kdiss.

Kinetic Constants for RSV Mabs

Mab	ka(assoc) $M^{-1}sec^{-1}$	kd(dissoc) sec-1	$t_{1/2}$# (Hrs)	K_d (k_d/k_a) nM
CH1129	5.0×10^4	7.5×10^{-5}	2.6	1.5
H1129	4.9×10^4	6.9×10^{-5}	2.8	1.4
M1129	3.5×10^4	4.0×10^{-4}	0.48	11.4
M1308F	3.5×10^4	3.8×10^{-5}	5.1	1.1
H1308F	2.2×10^4	5.5×10^{-5}	3.5	2.5

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